IN THE CLAIMS:

Please cancel Claims 1-15.

Please add the following claims.

16. A method for automatically analyzing nucleic acid data comprised of the

steps:

(a) performing an operation on a nucleic acid molecule;

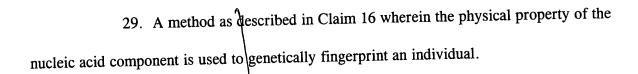
(b) generating data from the operation;

(c) representing the data as an electrical signal;

(d) operating on the electrical signal with a computing device to identify a subsignal corresponding to the operation; and

- (e) automatically analyzing the subsignal using a computing device to characterize a physical property of a nucleic acid component of the experiment.
- 17. A method as described in Claim 16 wherein the performing step (a) includes a polymerase chain reaction (PCR).
- 18. A method as described in Claim 17 wherein the performing step (a) includes PCR primers that are related to a genetic marker.
- 19. A method as described in Claim 18 wherein the genetic marker is polymorphic.
- 20. A method as described in Claim 19 wherein the automatic analyzing step
 (e) includes characterizing a size property of the nucleic acid component.
- 21. A method as described in Claim 20 wherein the genetic marker is a short tandem repeat.
 - 22. A method as described in Claim 17 wherein the PCR products are labeled.

- 23. A method as described in Claim 22 wherein the generating step (b) includes detecting the label.
- 24. A method as described in Claim 16 wherein the generating step (b) includes recording the electrical signal in the memory of a computer.
- 25. A method as described in Claim 22 wherein the representing step (c) includes recording the electrical signal as a label intensity relative to a time or space coordinate.
- 26. A method as described in Claim 16/wherein the operating step (d) includes locating the data in the subsignal within a prespective nucleic acid size range.
- 27. A method as described in Claim 16 wherein the analyzing step (e) includes characterizing a physical property corresponding to a molecular weight, nucleic acid size, nucleic acid quantity, nucleic acid concentration, or genome location.
- 28. A method as described in Claim 16 wherein the physical property of the nucleic acid component is used to positionally clone a gene.



- 30. A system for automatically analyzing nucleic acid data comprising:
- (a) means for performing an operation on a nucleic acid molecule;
- (b) means for generating data from the operation;
- (c) means for representing the data as an electrical signal;
- (d) means for operating on the electrical signal with a computing device to identify a subsignal corresponding to the operation; and
- (e) means for automatically analyzing the subsignal using a computing device to characterize a physical property of a nucleic acid component of the experiment.
 - 31. A system as described in Claim 30 wherein the operation is an experiment.

- 32. A method for automatically analyzing nucleic acid material of an organism comprised of the steps:
 - (a) obtaining nucleidacid material from the organism;
 - (b) amplifying a location of the material that includes a polymorphic region;
 - (c) determining a size property of the amplified location; and
- (d) automatically producing a genotype related to the size property of the amplified location of the nucleic acid material in an electronic acquisition system comprising a region having a radius of less than five feet at a rate exceeding 100 genotypes per hour.
- 33. A method as described in Claim 16 wherein the analyzing step (e) includes the step of exploiting a pattern in the data.